

SEQUENCE LISTING



(1) GENERAL INFORMATION:

- (i) APPLICANT: TAKESHI NAKAMURA
- (ii) TITLE OF INVENTION: HUMAN CYCLIN I AND GENES ENCODING SAME
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PILLSBURY, MADISON & SUTRO
 - (B) STREET: 1100 NEW YORK AVENUE, N.W.
 - (C) CITY: WASHINGTON
 - (D) STATE: D.C.
 - (E) COUNTRY: U.S.A.
 - (F) ZIP: 20005
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: FLOPPY DISK
 - (B) COMPUTER: IBM PC COMPATIBLE
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PATENTIN RELEASE #1.0, VERSION #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: U.S. 09/054,492
 - (B) FILING DATE: APRIL 3, 1998
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: PAUL E. WHITE, JR.
 - (B) REGISTRATION NUMBER: 32,011
 - (C) REFERENCE/DOCKET NUMBER: 7898/252159
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 861-3000
 - (B) TELEFAX: (202) 822-0944
 - (C) TELEX: 6714627CUSH

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Met Lys Phe Pro Gly Pro Leu Glu Asn Gln Arg Leu Ser Phe Leu
5 10 15
Leu Glu Lys Ala Ile Thr Arg Glu Ala Gln Met Trp Lys Val Asn
20 25 30

Val Arg Lys Met Pro Ser Asn Gln Asn Val Ser Pro Ser Gln Arg	35	40	45
Asp Glu Val Ile Gln Trp Leu Ala Lys Leu Lys Tyr Gln Phe Asn	50	55	60
Leu Tyr Pro Glu Thr Phe Ala Leu Ala Ser Ser Leu Leu Asp Arg	65	70	75
Phe Leu Ala Thr Val Lys Ala His Pro Lys Tyr Leu Ser Cys Ile	80	85	90
Ala Ile Ser Cys Phe Phe Leu Ala Ala Lys Thr Val Glu Glu Asp	95	100	105
Glu Arg Ile Pro Val Leu Lys Val Leu Ala Arg Asp Ser Phe Cys	110	115	120
Gly Cys Ser Ser Ser Glu Ile Leu Arg Met Glu Arg Ile Ile Leu	125	130	135
Asp Lys Leu Asn Trp Asp Leu His Thr Ala Thr Pro Leu Asp Phe	140	145	150
Leu His Ile Phe His Ala Ile Ala Val Ser Thr Arg Pro Gln Leu	155	160	165
Leu Phe Ser Leu Pro Lys Leu Ser Pro Ser Gln His Leu Ala Val	170	175	180
Leu Thr Lys Gln Leu Leu His Cys Met Ala Cys Asn Gln Leu Leu	185	190	195
Gln Phe Arg Gly Ser Met Leu Ala Leu Ala Met Val Ser Leu Glu	200	205	210
Met Glu Lys Leu Ile Pro Asp Trp Leu Ser Leu Thr Ile Glu Leu	215	220	225
Leu Gln Lys Ala Gln Met Asp Ser Ser Gln Leu Ile His Cys Arg	230	235	240
Glu Leu Val Ala His His Leu Ser Thr Leu Gln Ser Ser Leu Pro	245	250	255
Leu Asn Ser Val Tyr Val Tyr Arg Pro Leu Lys His Thr Leu Val	260	265	270
Thr Cys Asp Lys Gly Val Phe Arg Leu His Pro Ser Ser Val Pro	275	280	285
Gly Pro Asp Phe Ser Lys Asp Asn Ser Lys Pro Glu Val Pro Val	290	295	300
Arg Gly Thr Ala Ala Phe Tyr His His Leu Pro Ala Ala Ser Gly	305	310	315

Cys Lys Gln Thr Ser Thr Lys Arg Lys Val Glu Glu Met Glu Val
320 325 330

Asp Asp Phe Tyr Asp Gly Ile Lys Arg Leu Tyr Asn Glu Asp Asn
335 340 345

Val Ser Glu Asn Val Gly Ser Val Cys Gly Thr Asp Leu Ser Arg
350 355 360

Gln Glu Gly His Ala Ser Pro Cys Pro Pro Leu Gln Pro Val Ser
365 370 375

Val Met

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1133
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATG AAG TTT CCA GGG CCT TTG GAA AAC CAG AGA TTG TCT TTC CTG	45
TTG GAA AAG GCA ATC ACT AGG GAA GCA CAG ATG TGG AAA GTG AAT	90
GTG CGG AAA ATG CCT TCA AAT CAG AAT GTT TCT CCA TCC CAG AGA	135
GAT GAA GTA ATT CAA TGG CTG GCC AAA CTC AAG TAC CAA TTC AAC	180
CTT TAC CCA GAA ACA TTT GCT CTG GCT AGC AGT CTT TTG GAT AGG	225
TTT TTA GCT ACC GTA AAG GCT CAT CCA AAA TAC TTG AGT TGT ATT	270
GCA ATC AGC TGT TTT TTC CTA GCT GCC AAG ACT GTT GAG GAA GAT	315
GAG AGA ATT CCA GTA CTA AAG GTA TTG GCA AGA GAC AGT TTC TGT	360
GGA TGT TCC TCA TCT GAA ATT TTG AGA ATG GAG AGA ATT ATT CTG	405
GAT AAG TTG AAT TGG GAT CTT CAC ACA GCC ACA CCA TTG GAT TTT	450
CTT CAT ATT TTC CAT GCC ATT GCA GTG TCA ACT AGG CCT CAG TTA	495
CTT TTC AGT TTG CCC AAA TTG AGC CCA TCT CAA CAT TTG GCA GTC	540
CTT ACC AAG CAA CTA CTT CAC TGT ATG GCC TGC AAC CAA CTT CTG	585
CAA TTC AGA GGA TCC ATG CTT GCT CTG GCC ATG GTT AGT CTG GAA	630
ATG GAG AAA CTC ATT CCT GAT TGG CTT TCT CTT ACA ATT GAA CTG	675

CTT CAG AAA GCA CAG ATG GAT AGC TCC CAG TTG ATC CAT TGT CGG 720
 GAG CTT GTG GCA CAT CAC CTT TCT ACT CTG CAG TCT TCC CTG CCT 765
 CTG AAT TCC GTT TAT GTC TAC CGT CCC CTC AAG CAC ACC CTG GTG 810
 ACC TGT GAC AAA GGA GTG TTC AGA TTA CAT CCC TCC TCT GTC CCA 855
 GGC CCA GAC TTC TCC AAG GAC AAC AGC AAG CCA GAA GTG CCA GTC 900
 AGA GGT ACA GCA GCC TTT TAC CAT CAT CTC CCA GCT GCC AGT GGG 945
 TGC AAG CAG ACC TCT ACT AAA CGC AAA GTA GAG GAA ATG GAA GTG 990
 GAT GAC TTC TAT GAT GGA ATC AAA CGG CTC TAT AAT GAA GAT AAT 1035
 GTC TCA GAA AAT GTG GGT TCT GTG TGT GGC ACT GAT TTA TCA AGA 1080
 CAA GAG GGA CAT GCT TCC CCT TGT CCA CCT TTG CAG CCT GTT TCT 1125
 GTC ATG TA 1133

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CGTTCCCGGG TATGAAGTTT CCAGGGCCTT TGG

33

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

ACGGCTCGAG CTACATGACA GAAACAGGCT G

31

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Glu Asp Asn Val Ser Glu Asn Val Gly Ser Val Cys Gly Thr
5 10